



Identification of biomarkers to measure HIV-specific mucosal and systemic CD8⁺ T-cell immunity using single cell Fluidigm 48.48 Dynamic arrays

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ABSTRACT

Thirty genes composed of cytokines, chemokines, granzymes, perforin and integrins were evaluated in gut and splenic K^dGag_{197–205}-specific single CD8⁺ T cells using Fluidigm 48.48 Dynamic arrays, with the aim of identifying biomarkers to predict effective mucosal and systemic vaccine efficacy. The mRNA expression profiles were analyzed in three ways: (i) the “number” of K^dGag_{197–205}-specific CD8⁺ T cells expressing the biomarker, (ii) “level” of mRNA expression using principal component analysis (PCA) and (iii) poly-functionality in relation to RANTES expression. In total, 21 genes were found to be differentially expressed between the vaccine groups and the immune compartments tested. Overall, the PCA indicated that IL-13Rα2 or IL-4R antagonist adjuvanted vaccines that previously induced high-avidity mucosal/systemic CD8⁺ T cells with better protective efficacy, the “level” of mRNA expression, specifically RANTES, MIP-1β, and integrin α4 in gut K^dGag_{197–205}-specific single CD8⁺ T cells, were significantly elevated compared to unadjuvanted vaccine. Furthermore, significantly elevated granzymes/perforin levels were detected in IL-13^{−/−} mice given the unadjuvanted vaccine, indicating that the degree of IL-13 inhibition (total, transient or no inhibition) can considerably alter the level of T-cell activity/poly-functionality. When splenic- and gut-K^dGag_{197–205}-specific CD8⁺ T cells were compared, PC1 vs. PC2 scores revealed that not only RANTES, MIP-1β, and integrin α4 mRNA, but also perforin, granzymes A/B, and integrins β1 and β2 mRNA were elevated in spleen. Collectively, data suggest that RANTES, MIP-1β, perforin, and integrins α4, β1 and β7 mRNA in single HIV-specific CD8⁺ T cells could be used as a measure of effective mucosal and systemic vaccine efficacy.

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1. Introduction

Unlike mucosal vaccination, systemic vaccination induces CD8⁺ T cell that home poorly to the mucosae (e.g. the gut, genitourinary or the vaginal mucosae) [1–5]. Mucosal-associated lymphoid tissues are linked to what is known as the “common mucosal immune system”, whereby antigenic stimulation at one site can

result in immune responses in both local and distant mucosae, as a result of mucosal homing [6,7]. Homing of lymphocytes to specific tissues is driven by the expression of cell-surface adhesion molecules known as integrins or chemokine receptors. Integrins are composed of non-covalently linked α and β subunits [8] that have the ability to pair differentially to induce unique functions. α4β7 interacts with mucosal addressin cell adhesion molecule-1 (MAdCAM-1) expressed on capillary endothelial cells in the gastrointestinal mucosae [9] and αEβ7 interacts with E-cadherin expressed on intestinal epithelial cells [10]. Both these molecules can provoke lymphocyte homing to the gut mucosae [11–13]. Similarly, chemokine receptor CCR9 promotes cell homing to the small intestine by interacting with its receptor CCL25 (TECK), present on

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the intestinal epithelium. $\alpha 4\beta 1$ interacts with vascular cell adhesion molecule-1 (VCAM-1) and fibronectin [14,15]. $\alpha 4\beta 1$ -VCAM-1 binding can mediate firm adhesion of lymphocytes to the endothelium during blood cell extravasation and there is evidence that $\beta 1$ integrins can also mediate leukocyte retention, T-cell activation and homing to lung mucosae [16,17]. Similarly, $\beta 2$ integrins consisting of $\alpha L\beta 2$ (CD11a/CD18 or LFA-1), $\alpha M\beta 2$ (CD11b/CD18, Mac-1, CR3), $\alpha X\beta 2$ (CD11c/CD18, p150, 95, CR4) and $\alpha D\beta 2$ (CD11d/CD18) interact with intercellular adhesion molecule-1 (ICAM-1) and induce leukocyte adhesion, T-cell activation and homing to inflamed skin.

Until recently, IFN- γ production has been the main indicator of protective efficacy following vaccination, but many studies have now shown that IFN- γ expression alone does not always correlate with high avidity/quality CD8 $^{+}$ T cells and protective efficacy [2,18–22]. In recent studies, elevated numbers of high-avidity poly-functional HIV-specific T cells have been detected in HIV elite controllers compared to non-controllers [23–25], highlighting the importance of poly-functional CD8 $^{+}$ T cell immunity. In different studies, RANTES, MIP-1 α and MIP-1 β of the natural ligands for chemokine receptor 5 (CCR5) plus perforin and granzymes have been implicated in HIV-1 protective efficacy [26–31].

In the context of an HIV-1 vaccination, the induction of effective cytotoxic CD8 $^{+}$ T cells that migrate to the mucosae is thought to be of great importance in curtailing the infection. It is now well established that efficacy of a mucosal vaccine has to be assessed at the mucosae, not in the blood compartment. However, identifying markers that correlate with effective mucosal immunity has been a challenging task, which has hampered the design of effective mucosal vaccines for many mucosal pathogens. Specifically, difficulties associated with obtaining enough cells from mucosal tissue (e.g. gut, rectal, vaginal biopsies) have complicated the use of conventional techniques such as ELISpot and intracellular cytokine staining for measuring mucosal immunity [32]. Recently, the development of microfluidic devices (e.g. Fluidigm's integrated fluidic circuits and dynamic arrays) has enabled the measurement of multiple genes expression in antigen-specific single cells [33].

Surprisingly, no study to date has evaluated a comprehensive panel of integrins following mucosal HIV vaccination, especially at the single cell level. Thus, in this study, following intranasal/intramuscular HIV prime-boost vaccination, K d Gag_{197–205}-specific Peyer's patch and splenic single CD8 $^{+}$ T cells were sorted and the expression profiles of 30 different mRNAs composed of cytokines, chemokines, integrins, perforin and granzymes were analyzed. The mRNA expression profiles were evaluated in four vaccine conditions (including IL-13R $\alpha 2$ and IL-4R antagonist adjuvanted vaccines that have shown to induce high-avidity CD8 T cells [34,35]) using Fluidigm 48.48 Dynamic array with the aim of identifying surrogate mucosal-specific biomarkers that would effectively measure mucosal immunity.

2. Materials and methods

2.1. Immunization of mice and mucosal/systemic lymphocytes preparation

Pathogen-free 6–8-week-old female BALB/c WT and BALB/c IL-13 KO mice were prime-boost immunized with i.n. FPV-HIV/i.m.VV-HIV unadjuvanted vaccine strategy or IL-13R $\alpha 2$ -adjuvant or IL-4R antagonist adjuvant vaccine strategies as in Table 1 [34,35], under isoflurane anesthesia two weeks apart similar to our previous studies [2,22,34,35]. To measure systemic and mucosal immune responses, mice were euthanized at 2 weeks post-booster vaccination; spleen and Peyer's patches were removed and single cell suspensions were prepared as described previously [35,36].

Table 1

Mice and prime-boost vaccine strategies used in this study.

| | Mice | Prime | Boost |
|---|------------------|--|---|
| 1 | BALB/c | i.n. FPV-HIV | i.m. VV-HIV |
| 2 | IL-13 $^{-/-}$ * | i.n. FPV-HIV | i.m. VV-HIV |
| 3 | BALB/c | i.n. FPV-HIV-IL-13R $\alpha 2\Delta 10$ ** | i.m. VV-HIV-IL-13R $\alpha 2\Delta 10$ ** |
| 4 | BALB/c | i.n. FPV- HIV-IL-4C118** | i.m. VV- HIV-IL-4C118** |

All recombinant fowlpox virus (rFPV) and recombinant vaccinia virus (rVV) constructs encode HIV-1 gag/pol antigens. i.n. intranasal, i.m. intramuscular. The i.n. rFPV was given in a final volume of 20–25 μ l, where i.m. rVV immunization was delivered in a 100 μ l volume. All viruses were diluted in sterile phosphate-buffered saline (PBS) and then sonicated, to obtain homogeneous viral suspensions before delivery.

Note. In previous studies *IL-13 $^{-/-}$ mice given the control unadjuvanted vaccine strategy [22] and **BALB/c mice given the IL-13R $\alpha 2$ adjuvanted (IL-13R $\alpha 2\Delta 10$) or IL-4R antagonist adjuvanted (IL-4C118) HIV vaccines that transiently inhibit IL-4 and/or IL-13 were found to induce mucosal and systemic K d Gag_{197–205}-specific CD8 $^{+}$ T cells of higher avidity which was associated with greater cell mediated protective efficacy compared to BALB/c mice given the control unadjuvanted vaccine [34,35] (avidity profiles were IL13 $^{-/-}$ unadjuvanted > BALB/c adjuvanted > BALB/c unadjuvanted).

2.2. Tetramer and homing markers staining

Allophycocyanin (APC) conjugated K d Gag_{197–205} tetramers were synthesized at the Bio-Molecular Resource Facility at JCSMR/ANU. Tetramer staining was performed as described previously [2,37]. Briefly, 2×10^6 splenocytes and mucosal lymphocytes were stained with anti-CD8-FITC antibody (BD PharMingen, San Diego, CA) and APC conjugated K d Gag_{197–205} tetramer at room temperature for 40 min. To evaluate homing markers by flow cytometry (FACS), following tetramer staining cells were also surface stained with biotin labeled anti-mouse $\alpha 4\beta 7$ (e-Biosciences, USA), PE conjugated anti-mouse $\alpha L\beta 2$ (Biolegend, USA), FITC conjugated anti-mouse CCR9 (Biolegend, USA) and/or anti-mouse CD29/ $\beta 1$ (Biolegend, USA) antibodies for 25 min at 4 $^{\circ}$ C, followed by brilliant violet 421 streptavidin (Biolegend, USA) for 25 min at 4 $^{\circ}$ C. Cells were fixed and total 10^6 events per sample were collected using Fortessa flow cytometer (Becton-Dickinson), and results were analyzed using Cell Quest Pro software.

2.3. Evaluation of single-cell mRNA expression profiles using Fluidigm 48.48 Dynamic arrays

K d Gag_{197–205} tetramer $^{+}$ CD8 $^{+}$ single cells from spleen and Peyer's patches were sorted¹ using cell FACS Aria I (BD Biosciences) into 96-well plates containing CellsDirect qRT-PCR reaction buffer (Invitrogen), Platinum Taq polymerase/SuperScript III reverse transcriptase (Invitrogen), a mixture of Taqman primer-probes at 0.2 \times concentration specific for the transcripts of interest, as listed in Supplementary Table 1 (Applied Biosystems), and Superscript RNase inhibitor. Immediately following cell sorting, samples were centrifuged, and subjected to 20 cycles of pre-amplification using polymerase chain reaction (PCR) (cell cycling as: 1 \times 50 $^{\circ}$ C 15 min for the reverse transcription, 1 \times 95 $^{\circ}$ C 2 min for reverse transcriptase inactivation and Taq polymerase activation, followed by 20 cycles 95 $^{\circ}$ C 15 s and 60 $^{\circ}$ C 4 min amplification cycle). Subsequently, the pre-amplified single-cell cDNA was stored at –20 $^{\circ}$ C until analysis and was diluted with dH $_2$ O (1:2) prior to qPCR reaction. Each pre-amplified cDNA sample was then separated into 48 separate reactions for qPCR analysis using the

¹ NOTE: The purity of these cells was 99% as stringent gating was used to determine CD8 $^{+}$ tetramer $^{+}$ cells as done in our previous studies in spleen [2,35] and Peyer's patches [35,68]. Also, non HIV-specific tetramer is used as a negative control to clearly established that the double positive cells detected are true HIV-specific CD8 T cells.

BioMark 48.48 Dynamic array nanofluidic chip (Fluidigm Inc., USA) according to manufacturer's instruction (see [Supplementary Fluidigm section](#) for chip loading).

2.4. Statistical analysis

Amplification signals were analyzed and C_t values were determined using Fluidigm's real-time PCR analysis software version 4. In a preliminary analysis, C_t values were dichotomised based on the presence/absence of gene expression and the number of cells expressing a particular gene [38] in the groups indicated in [Supplementary Table 1](#) were then compared using Fisher's exact test with SPSS (Statistical Package for the Social Sciences, International Business Machine Corp., USA) version 21.0 [39]. Principal components analysis (PCA) was used to assess patterns of mRNA expression levels of genes, and expression level/poly-functionality was analyzed using a Matlab software package [40] (see [Supplementary information](#) section for more details). FACS data the standard error of the mean and p values were determined using one-way analysis of variance followed by Bonferroni's post tests for comparison of selected pairs in GraphPad Prism software version 5.

3. Results

3.1. IL-13 α 2 and IL-4R antagonist adjuvanted HIV vaccines can induce distinct mRNA expression profiles in gut-K^dGag_{197–205}-specific CD8⁺ T cells

The gut-K^dGag_{197–205}-specific single cells obtained from novel IL-13 α 2 and IL-4R antagonist adjuvanted HIV vaccinated groups showed distinct mRNA expression profiles ([Supplementary Fig. 1c and d](#)) compared to the WT or IL-13 KO animals that received the standard unadjuvanted vaccination ([Supplementary Fig. 1a and b](#)). Unlike cytokine expression, selected chemokines/their receptors, perforin, granzymes and integrin expression patterns were significantly different between the four vaccination groups tested.

Firstly, when quantitative analysis was performed as a percentage of single gut K^dGag_{197–205}-specific CD8⁺ T cells expressing the mRNAs of interest, at the chemokine level mRNA expression hierarchy of RANTES > MIP-1 β > MIP-1 α was detected between the four vaccination groups tested ([Fig. 1a](#)). The number of RANTES expressing gut K^dGag_{197–205}-specific CD8⁺ cells was significantly higher in the IL-4R antagonist adjuvanted vaccinated group (83%) and the IL-13 KO mice (89%) given the unadjuvanted vaccine compared to the WT BALB/c mice (66%) (unadjuvanted vaccine vs. IL-13 KO $p=0.008$; unadjuvanted vaccine vs. IL-4R antagonist vaccine $p=0.016$) ([Fig. 1a](#)). The CCR5 also displayed a similar expression profile to RANTES where unadjuvanted vaccine vs. IL-13 KO $p=0.001$; unadjuvanted vaccine vs. IL-4R antagonist vaccine $p=0.019$ ([Fig. 1a](#)). Even though no statistical significance was observed, IL-13 α 2 adjuvanted group also showed greater increase in both RANTES and CCR5 compared to the control unadjuvanted group.

Next, when the numbers of granzymes and perforin expressing cells (critical mediators of anti-viral cytotoxic immunity) were evaluated, 10–40% gut K^dGag_{197–205}-specific CD8⁺ T cells were found to express granzymes A and B, while 60–80% expressed perforin, and no granzyme C was detected in all four groups tested, where the expression hierarchy was perforin > granzymes A and B ([Fig. 1b](#)). Interestingly, the perforin mRNA expression profile was significantly different between WT mice and IL-13 KO mice that received the unadjuvanted vaccine ($p=0.009$) unlike the group that received the adjuvanted vaccines ([Fig. 1b](#)).

Unlike transient inhibition of IL-13 (IL-13 α 2 adjuvanted vaccine), the complete absence of IL-13 (e.g. IL-13 KO mice) significantly reduced the number of gut K^dGag_{197–205}-specific CD8⁺ T cells expressing the memory differentiation marker CD62L (L-selectin/Sell) (WT vs. IL-13 KO $*p=0.020$) and activation marker CD69 (WT vs. IL-13 KO $**p=0.002$) ([Fig. 1c](#)), but enhanced expression of P-selectin ligand or Selp1g (WT vs. IL-13 KO $*p=0.017$) were detected. No significant differences in CD62L, P-selectin ligand, CCR7 or CD69 mRNA expression were found in BALB/c mice given the unadjuvanted or adjuvanted vaccines ([Fig. 1c](#)).

3.2. IL-13 inhibition can induce distinct integrin mRNA expression profiles in gut-K^dGag_{197–205}-specific CD8⁺ T cells

Since an effective vaccine against HIV-1 should have the ability to recruit antigen-specific effector CD8⁺ T cells to the mucosae, next the integrin expression profiles were evaluated. Knowing that α 4 can heterodimerize with either β 7 or β 1, while α E can only heterodimerize with β 7, when these integrins were evaluated in gut K^dGag_{197–205}-specific CD8⁺ cells, α 4 and β 7 mRNA were detected in 60–90% of the cells from all groups tested ([Fig. 1d](#)). β 1 mRNA expression was similar between the BALB/c mice that received the unadjuvanted or adjuvanted vaccines (~40%) ([Fig. 1d](#)). However, the IL-13 KO animals that received the unadjuvanted vaccination showed significantly elevated numbers of cells expressing α 4 and β 1 mRNA (WT vs. IL-13 KO, $*p=0.014$; WT vs. IL-13 KO, $*p=0.017$) and significantly reduced numbers of cells expressing α E were detected (WT vs. IL-13 KO, $*p=0.012$) compared to the wild type animals that received the same vaccine ([Fig. 1d](#)).

β 2 integrin is known to heterodimerize with α D, α L, α M or α X. Our data revealed that out of these integrins, only α L and α X mRNA were detected in gut K^dGag_{197–205}-specific CD8⁺ T cells ([Fig. 1e](#)). The number of gut K^dGag_{197–205}-specific CD8⁺ T cells that expressed α L and β 2 mRNA was significantly lower in IL-4R antagonist adjuvanted group compared to the BALB/c mice that received the unadjuvanted vaccine ($*p=0.03$) ([Fig. 1e](#)). Also very low numbers of cells were found to express in α X mRNA in all groups tested with no significant difference.

3.3. Quantitatively distinct mRNA expression profiles were observed following novel adjuvanted vaccination compared to unadjuvanted control vaccine strategy

To establish the qualitative differences in log mRNA expression and to identify potential mucosal-specific CD8⁺ T-cell biomarkers, next the mRNA expression levels in single gut-K^dGag_{197–205}-specific CD8⁺ T cells were detected using a multivariate PCA approach (see [Supplementary statistics section](#) for details). In this analysis, the rank-correlated expression ([Fig. 2a](#)) of 21 mRNAs was best approximated by the four principal components (PC1, PC2, PC3 and PC4) that explained at least 75% of the total variance.

The first principal component (PC1) explained 36% of the total variance in overall log expression. This axis reflected the pattern of positively correlated expression of RANTES, MIP1 β , perforin, CCR5 and integrin α 4 and negatively correlated expression of CCR9, CCR7 and Sell/L-selectin ([Fig. 2b](#)). PC1 scores differentiated the adjuvanted vaccine groups which had higher relative expression of RANTES, MIP1 β , and integrin α 4 and correspondingly lower relative expression of CCR9, CCR7, Sell/L-selectin and integrin α E, from the unadjuvanted vaccine group ($p<0.001$) ([Fig. 2b–d](#)).

The second principal component (PC2) explained 18% of the total variation in overall log expression. This axis reflected the coordinated expression of MIP1 α , MIP1 β , RANTES, CCR5, granzymes A and B, TNF- α and IFN- γ ([Fig. 2b](#)). Mean PC2 scores differed significantly between the IL-13 KO and other vaccine groups with IL-13 KO mice showing increased expression patterns of MIP1 α , MIP1 β ,

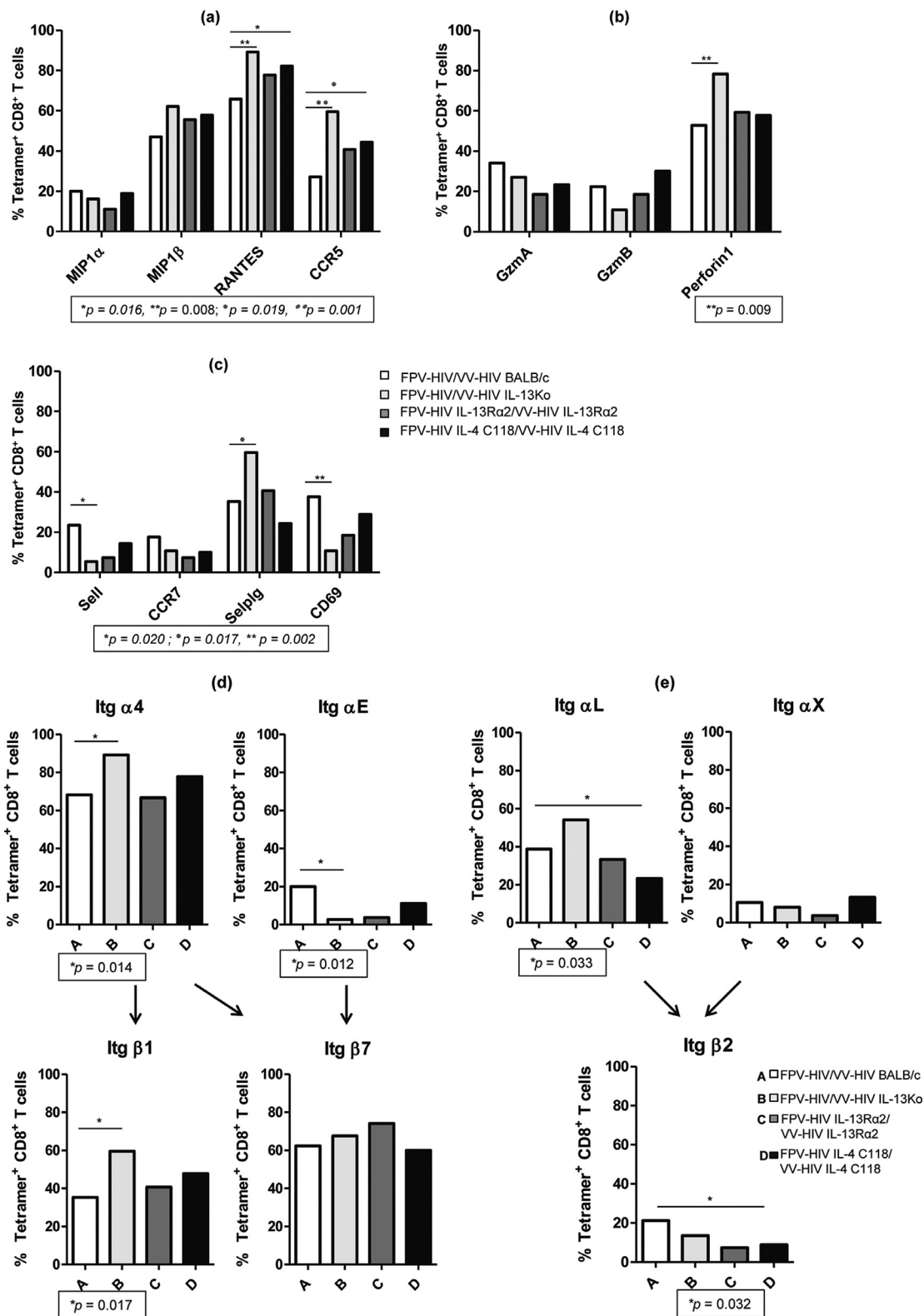


Fig. 1. Detailed evaluation of percentage of mucosal K^dGag_{197–205} tetramer⁺ CD8⁺ single cells expressing particular gene in different vaccine groups compared to the standard FPV-HIV/VV-HIV vaccine. Wild type (WT) BALB/c and IL-13 gene knock out (KO) mice (*n* = 4–5) were immunized (i.n./i.m.) with vaccines indicated in Table 1. Fourteen days post boost immunization tetramer staining of Peyer's patch samples was performed, K^dGag_{197–205}-specific CD8⁺ single cells were sorted into 96-well plate (total 48 cells per group), and cDNA was synthesized followed by single cell gene expression analysis using Fluidigm's BiomarkTM real-time PCR system (Supplementary Table 1). The graphs represent the percentages of K^dGag_{197–205} tetramer⁺ CD8⁺ single cells (y-axis) in Peyer's patches expressing MIP1 α , MIP1 β , RANTES and CCR5 (a), granzyme A, granzyme B, perforin1 (b), sell/CD62L, CCR7, selp1g/P-selectin ligand and CD69 (c). The graph also shows percentage of K^dGag_{197–205}-specific CD8⁺ T cells expressing integrins (d, e) in different vaccine groups. The *p* values were determined using Fisher's exact statistical test (note: **p* values in the box are for genes mentioned left to right on x-axis). Data represent two experiments for standard unadjuvanted vaccine and IL-4R antagonist adjuvanted vaccine and one experiment for IL-13 KO and IL-13R α 2 adjuvant vaccine group. Note: in this study, where less than 10% of the single cells expressed the mRNA of interest, they were excluded from further analysis (example: IL-2, IL-4, IL-13, IL-17, CCR10, granzyme C, and integrins α M and α D).

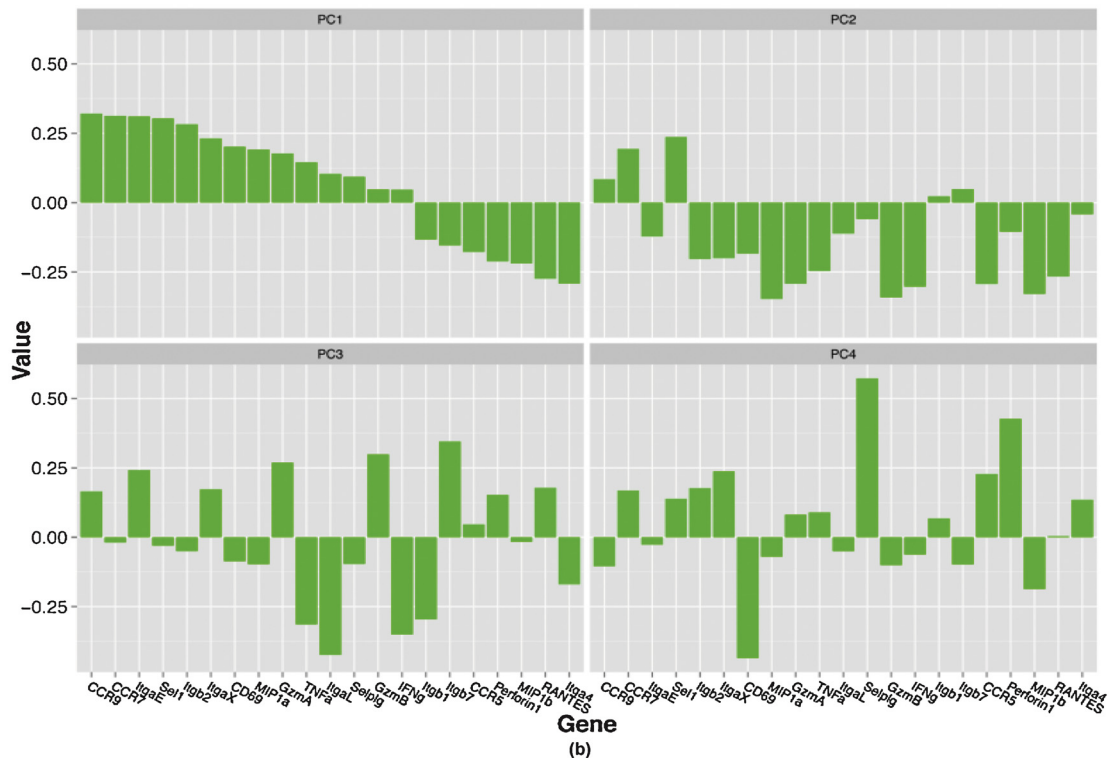
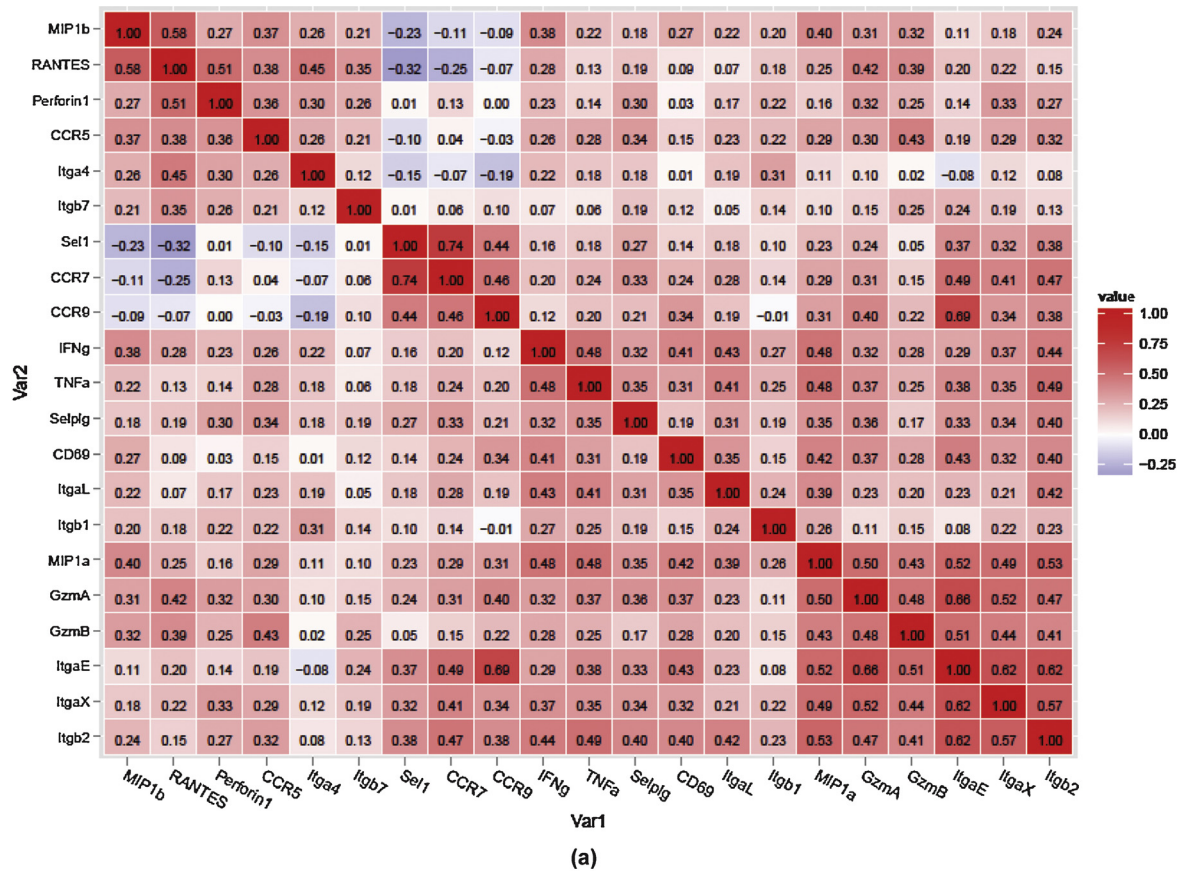


Fig. 2. PCA of K^dGag_{197–205}-specific single CD8⁺ T cell gene expression patterns in Peyer's patches following different vaccinations. The rank-correlated expression of 21 mRNA's (a) and the genes contribution in each principle component are shown (b). The co-expression levels of gene transcripts within single K^dGag_{197–205}-specific CD8⁺ T cell were analyzed in PC1 vs. PC2 component (c), PC1 vs. PC4 component (d) and PC1 vs. PC3 component (e). In each PCA plot the dot represents K^dGag_{197–205}-specific single CD8⁺ T cell (red: FPV-HIV IL-4C118/VV-HIV IL-4C118, $n = 86/96$ single cells; green: FPV-HIV IL-13R α 2/VV-HIV IL-13R α 2, $n = 27/48$ single cells; blue: FPV-HIV/VV-HIV IL-13 KO, $n = 37/48$ single cells; black: FPV-HIV/VV-HIV BALB/c, $n = 83/96$ single cells). The bold bigger dots represent mean gene expression level for different vaccine groups tested; analysis of variance (ANOVA) was used to compare the primary principal component scores across the groups as mentioned in Section 2. Data represent two experiments for standard unadjuvanted vaccine and IL-4R antagonist adjuvanted vaccine and one experiment for IL-13 KO and IL-13R α 2 adjuvant vaccine group. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of the article.)

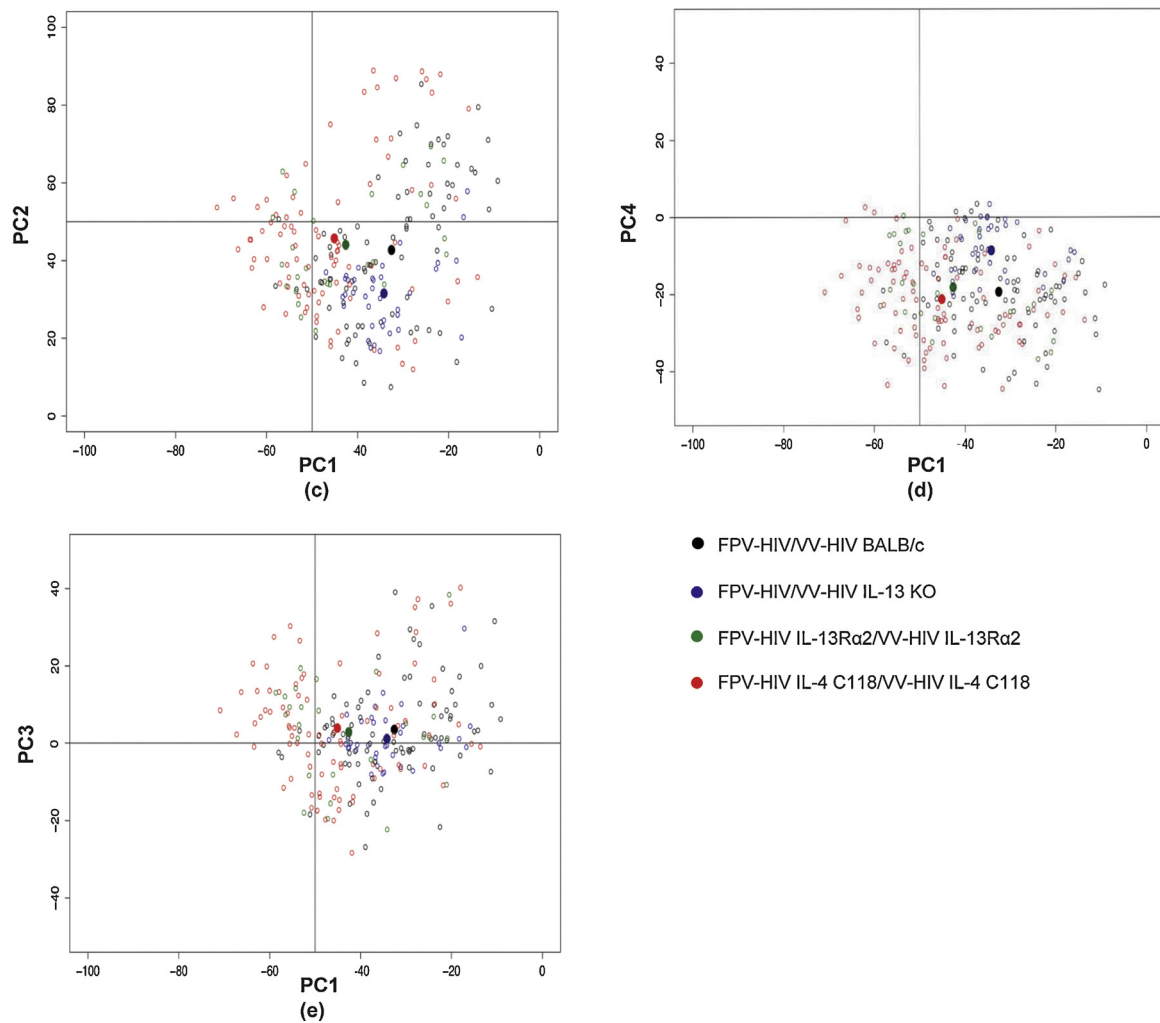


Fig. 2. (Continued).

RANTES, CCR5, granzymes A and B, TNF- α and IFN- γ compared with the other groups ($p < 0.001$) (Fig. 2c). The fourth principal component (PC4) likewise described significant differences between IL-13 KO and other vaccine groups tested and corresponded to relative low expression of CD69 and high expression of P-selectin ligand (Selplg) and perforin mRNA in IL-13 KO vaccinated group ($p < 0.01$) (Fig. 2b and d). The third principal component (PC3) corresponded with no significant differences between all the groups tested (Fig. 2e).

Overall, our PCA results indicated that (i) following novel IL-13Rα2 or IL-4R antagonist adjuvanted vaccination, the “level” of mRNA expression (specifically RANTES, MIP-1 β , and integrin $\alpha 4$) in gut K^dGag_{197–205}-specific single CD8⁺ T cells was significantly elevated compared to unadjuvanted control vaccine and (ii) the mRNA expression patterns in animals which received IL-13Rα2 or IL-4R antagonist adjuvanted vaccines showed significantly different mRNA expression profiles to that of IL-13 KO mice.

3.4. Distinct mRNA expression profiles were detected in systemic and mucosal K^dGag_{197–205}-specific single CD8⁺ T cells

With the goal of identifying possible surrogate markers of effective mucosal immunity in the systemic compartment, next splenic and Peyer’s patch K^dGag_{197–205}-specific single CD8⁺ T cells were analyzed between unadjuvanted and IL-4R antagonist vaccinated groups. Data revealed that the numbers of K^dGag_{197–205}-specific

CD8⁺ T cells that expressed RANTES and granzyme A mRNA were significantly higher in spleen while CD62L and CD69 were significantly higher in Peyer’s patch (Fig. 3a). Additionally, the IL-4R antagonist adjuvanted vaccinated group also showed significantly elevated numbers: K^dGag_{197–205}-specific CD8⁺ T cells expressing perforin ($p = 0.03$) and MIP-1 α mRNA ($p = 0.027$) in spleen and Peyer’s Patch, respectively (Fig. 3a). Similarly, in the unadjuvanted vaccine group, Granzyme B ($p = 0.021$) and CCR7 ($p = 0.0001$) mRNA expression was significantly higher in gut K^dGag_{197–205}-specific CD8⁺ T cells compared to spleen. Also in gut CD62L⁺ CCR7⁺ effector memory (Em) phenotype was greater (80%) than CD62L⁺ CCR7⁺ central memory (Cm) K^dGag_{197–205}-specific CD8⁺ T-cell phenotype (20%), no Cm CD8 T cells were detected in spleen (Fig. 3a).

3.5. Distinct integrin/CCR9 mRNA and protein expression profiles were detected in systemic and mucosal K^dGag_{197–205}-specific single CD8⁺ T cells

Knowing $\alpha 4$ can heterodimerize with $\beta 7$ and $\beta 1$ while αE can only heterodimerize with $\beta 7$, next mRNA expression profiles of these integrins in spleen and Peyer’s patch K^dGag_{197–205}-specific single CD8⁺ T cells were evaluated. In both compartments, integrins $\alpha 4$ (80–90%) and $\beta 7$ (50–70%) expressions were found to be similar following unadjuvanted and IL-4R antagonist adjuvanted vaccination (Fig. 3b). However, compared to Peyer’s patch significant increase in the number of splenic K^dGag_{197–205}-specific single CD8⁺

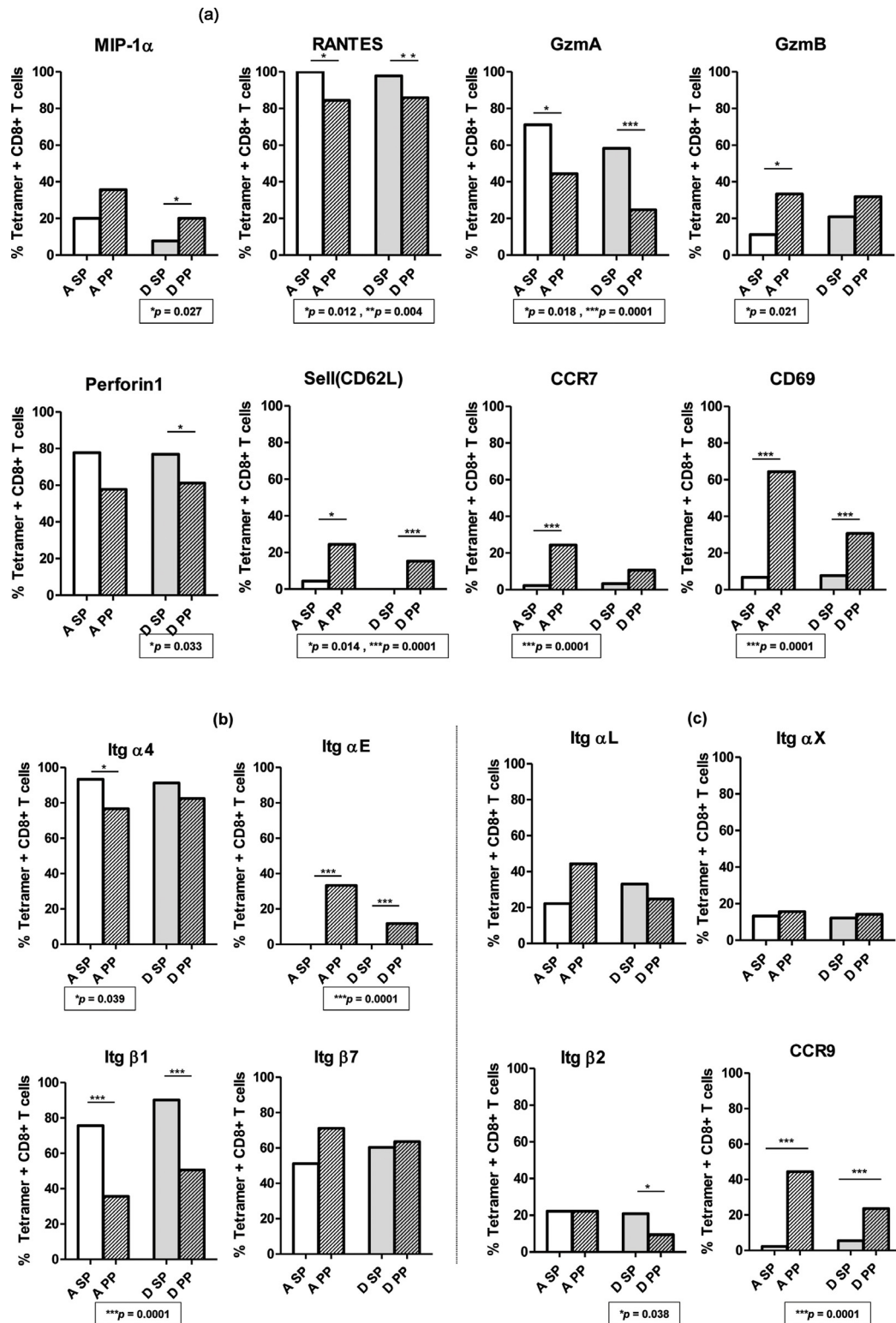


Fig. 3. Evaluation of percentage of K^d Gag_{197–205}-specific single CD8⁺ T cell expressing genes in systemic and mucosal compartments. BALB/c mice ($n=5$ per group) were immunized i.n./i.m. with standard FPV-HIV/VV-HIV vaccine or FPV-HIV IL-4C118/VV-HIV IL-4C118 vaccine. Fourteen days post boost immunization, spleen and Peyer's patches were harvested and single-cell suspensions prepared; following tetramer staining K^d Gag_{197–205}-specific single splenic and Peyer's patch CD8⁺ T cells (total of 48 cells) were sorted from the same group of animals, cDNA was synthesized and mRNA expression was evaluated using Fluidigm Biomark™ real-time PCR system as mentioned in Section 2. The graphs (a–c) represent percentage of K^d Gag_{197–205}-specific single CD8⁺ T cell expressing indicated genes, the x-axis A SP and A PP = spleen and Peyer's patches of FPV-HIV/VV-HIV vaccinated group, D SP and D PP (gray filled) = spleen and Peyer's patches of FPV-HIV IL-4C118/VV-HIV IL-4C118 vaccinated group. Following standard or novel vaccination, the percentages of tetramer-specific single CD8⁺ T cells expressing particular gene were compared between spleen and Peyer's patches; significant differences as indicated by p -values below the graphs were determined using Fisher exact's test. Standard unadjuvanted vaccine represents one experiment and IL-4R antagonist adjuvanted vaccine represents data from two experiments. The spleen and Peyer's patches were harvested from same experiment and the statistical significance is shown between the two compartments within a vaccination group.

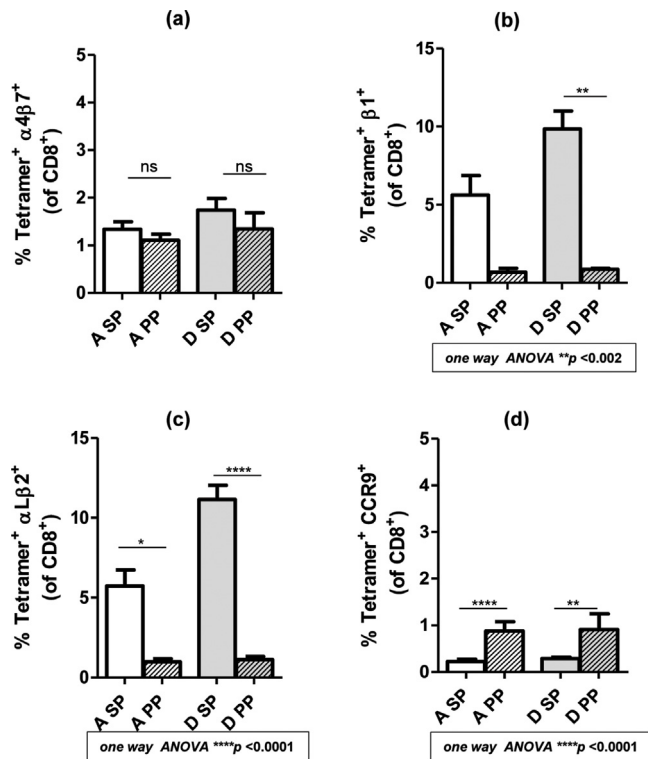


Fig. 4. Evaluation of integrin protein expression in K^dGag_{197–205}-specific CD8⁺ T cells in spleen and Peyer's patches using flow-cytometry. BALB/c mice ($n = 4$ per group) were immunized i.n./i.m. with standard unadjuvanted vaccine or IL-4R antagonist adjuvanted vaccine, 14 days post boost immunization spleen and Peyer's patches were collected (note: Peyer's patches were pooled from all animals), tetramer and homing marker staining was performed as mentioned in Section 2, and the percentages of K^dGag_{197–205}-specific CD8⁺ T cells that expressed integrin α4β7 (a), β1 (b), αLβ2 (c), and CCR9 (d) were analyzed in spleen and Peyer's patches using flow-cytometry. The x-axis A SP and A PP = spleen and Peyer's patches of FPV-HIV/VV-HIV vaccinated group, D SP and D PP (gray filled) = spleen and Peyer's patches of FPV-HIV IL-4C118/VV-HIV IL-4C118 vaccinated group, error bars indicate standard error of mean, the p values for multiple comparisons were obtained from one-way analysis of variance followed by Bonferroni's post hoc tests. Data for gut-specific homing markers expression α4β7 and CCR9 by tetramer⁺ CD8⁺ T cells represent average of 5–7 experiments and for integrins αLβ2 and β1 represent 2–3 experiments. Note: % K^dGag_{197–205}-specific CD8⁺ T cells in spleen = 5–6% for standard FPV-HIV/VV-HIV vaccine and 10–12% for IL-4R antagonist vaccine; % K^dGag_{197–205}-specific CD8⁺ T cells in Peyer's patches = 0.5–1.5% for standard FPV-HIV/VV-HIV vaccine and 2–3% for IL-4R antagonist vaccine consistent to our previous studies [34,35].

T cells that expressed integrin β1 mRNA was detected ($p < 0.0001$) (Fig. 3b) while, higher numbers of integrin αE mRNA expressing cells were detected in Peyer's patch compared to spleen ($p < 0.0001$) (Fig. 3b) in both vaccine groups tested.

We next assessed mRNA expression of αL and αX which are known to heterodimerize with integrin β2. Although data revealed that αL and αX were not significantly different between spleen and Peyer's patch in both vaccine groups tested (Fig. 3c), compared to Peyer's patch there was a significant increase in the number of splenic K^dGag_{197–205}-specific single CD8⁺ T cells that expressed integrin β2 mRNA in IL-4R antagonist vaccinated group ($p = 0.038$) (Fig. 3c). In addition to integrins, in both vaccine groups, K^dGag_{197–205}-specific CD8⁺ T cells that expressed the CCR9 were significantly elevated in Peyer's patch compared to spleen ($p = 0.0001$) (Fig. 3c). Flow cytometry analysis of K^dGag_{197–205}-specific CD8⁺ T cells revealed that similar to what was observed at the mRNA level (Fig. 3a), no significant differences in heterodimer α4β7 were detected between spleen and Peyer's patches in both vaccines tested (Fig. 4a). In the IL-4R antagonist vaccine group, the number K^dGag_{197–205}-specific CD8⁺ T cells that expressed β1

were elevated in spleen compared to Peyer's patch (Fig. 4b). Moreover, although there was no significant difference in αL mRNA in spleen and Peyer's patch, the numbers of αLβ2 expressing splenic K^dGag_{197–205}-specific CD8⁺ T cells were significantly elevated in both vaccine groups tested (Fig. 4c). Our data also indicated that unlike α4β7, the number of K^dGag_{197–205}-specific CD8⁺ T cells that expressed CCR9 were significantly elevated in Peyer's patch compared to spleen at both the mRNA (Fig. 3c) and protein level (Fig. 4d), suggesting that CCR9 is more specific to gut. Collectively, the single-cell mRNA expression analysis and flow cytometry analysis clearly indicated that following vaccination distinct gene expression profiles can be observed in systemic and mucosal K^dGag_{197–205}-specific CD8⁺ T cells.

3.6. PCA revealed distinct mRNA expression profiles between systemic and mucosal compartments

Next PCA was performed to evaluate the differences between spleen and Peyer's patch. In this analysis, the rank-correlated expression (Fig. 5a) of 21 mRNAs was best approximated by four principal components (PC1, PC2, PC3, PC4) that explained at least 71.5% of the total variance. The PC1 explained 38% of the total variance in overall log expression. This axis reflected the coordinated expression of perforin, integrin α4 and β1 and also of CD69, CCR9, MIP-1α, Sell/L-selectin and CCR7 mRNA (Fig. 5b). PC1 scores differentiated the spleen which had relatively higher expression of perforin, integrin α4 and β1 and lower expression of CD69, CCR9, MIP-1α, Sell/L-selectin and CCR7 from the Peyer's patches of respective vaccine groups ($p < 0.001$) (Fig. 5c). Mean PC1 scores also differentiated adjuvanted vaccine group which had relatively higher expression of perforin, integrin α4 and β1 in splenic K^dGag_{197–205}-specific CD8⁺ T cells from the unadjuvanted group ($p < 0.01$) (Fig. 5c).

The PC2 explained 18% of the total variance in overall log expression. This axis reflected the coordinated mRNA expression profile of RANTES, MIP-1β, granzyme A and B and integrin β2 (Fig. 5b). Mean PC2 scores differed significantly between spleens and Peyer's patch with relatively higher expression of this profile in spleen ($p < 0.001$) (Fig. 5c). The PC3 explained only 8% of the total variance in overall log expression. Mean PC3 scores differed significantly between spleen and Peyer's patch and indicated relatively higher expression of integrin αL and lower expression of integrin β7 in spleen compared to Peyer's patches of respective vaccine groups (Fig. 5d). The PC4 corresponded with no significant differences between spleen and Peyer's patches (Fig. 5e).

3.7. The gut K^dGag_{197–205}-specific CD8⁺ T cells that expressed RANTES were polyfunctional

As relatively higher proportion of gut K^dGag_{197–205}-specific CD8⁺ T cells expressed RANTES in all the three groups when compared to the unadjuvanted vaccination (Fig. 1a), we next evaluated the probability of other mRNAs to co-express together with RANTES (polyfunctionality in relation to RANTES) using the Matlab script that was developed. Data indicated that more than 50% of RANTES expressing gut K^dGag_{197–205}-specific CD8⁺ T cells obtained from (i) BALB/c mice given the unadjuvanted vaccine co-expressed MIP1-β, perforin, granzyme-A, integrin α4 and β7 (Fig. 6a), (ii) IL-13 KO mice given the unadjuvanted vaccine co-expressed MIP1-β, CCR5, perforin, P-selectin ligand, integrin α4, αL, β1 and β7 (Fig. 6b), (iii) FPV-HIV IL-13Rα2/VV-HIV IL-13Rα2 adjuvanted vaccinated group co-expressed MIP1-β, perforin, integrin α4 and β7 (Fig. 6c) and (iv) FPV-HIV IL-4C118/VV-HIV IL-4C118 adjuvanted vaccinated group co-expressed MIP1-β, perforin, CCR5, integrin α4, β1 and β7 (Fig. 6d). In FPV-HIV/VV-HIV and FPV-HIV IL-4C118/VV-HIV IL-4C118 vaccinated groups, K^dGag_{197–205}-specific splenic CD8⁺ T

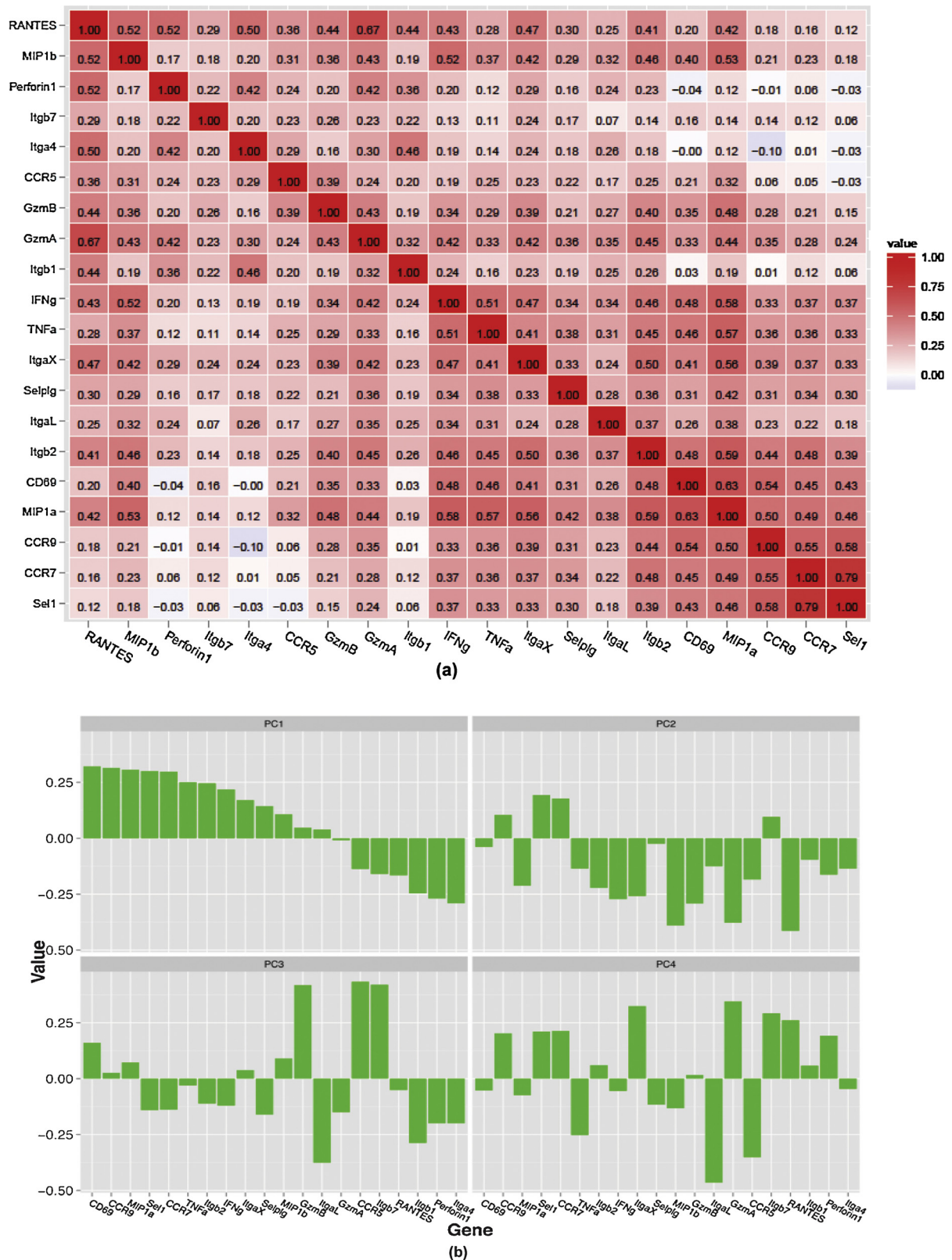


Fig. 5. PCA of K^dGag₁₉₇₋₂₀₅-specific single CD8⁺ T-cell gene expression patterns in spleen vs. Peyer's patches. Following standard vaccine and/IL-4R antagonist adjuvanted vaccination mRNA expression levels were compared in between the two tissues. The rank-correlated expression of 21 mRNA's (a) and the genes contribution in each principle component are shown (b). In PC1 vs. PC2 plot (c), PC1 vs. PC3 plot (d) and PC1 vs. PC4 plot (e) the dots represent K^dGag₁₉₇₋₂₀₅-specific single CD8⁺ T cells isolated from Peyer's patches and triangles represent K^dGag₁₉₇₋₂₀₅-specific single CD8⁺ T cells isolated from spleen. The cluster of mean gene expression levels is indicated as filled black dot: Peyer's patch K^dGag₁₉₇₋₂₀₅-specific CD8⁺ T-cell response after FPV-HIV/VV-HIV vaccination ($n=45/48$ single cells); filled red dot: Peyer's patch K^dGag₁₉₇₋₂₀₅-specific CD8⁺ T cell response after FPV-HIV IL-4C118/VV-HIV IL-4C118 vaccination ($n=86/96$ single cells); filled blue triangle and yellow triangle for K^dGag₁₉₇₋₂₀₅-specific CD8⁺ T cell response in spleen following FPV-HIV/VV-HIV ($n=45/48$ single cells) and/FPV-HIV IL-4C118/VV-HIV IL-4C118 vaccination ($n=91/96$ single cells), respectively. Data represent one experiment with standard vaccine and two experiments with IL-4R antagonist vaccine. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of the article.)

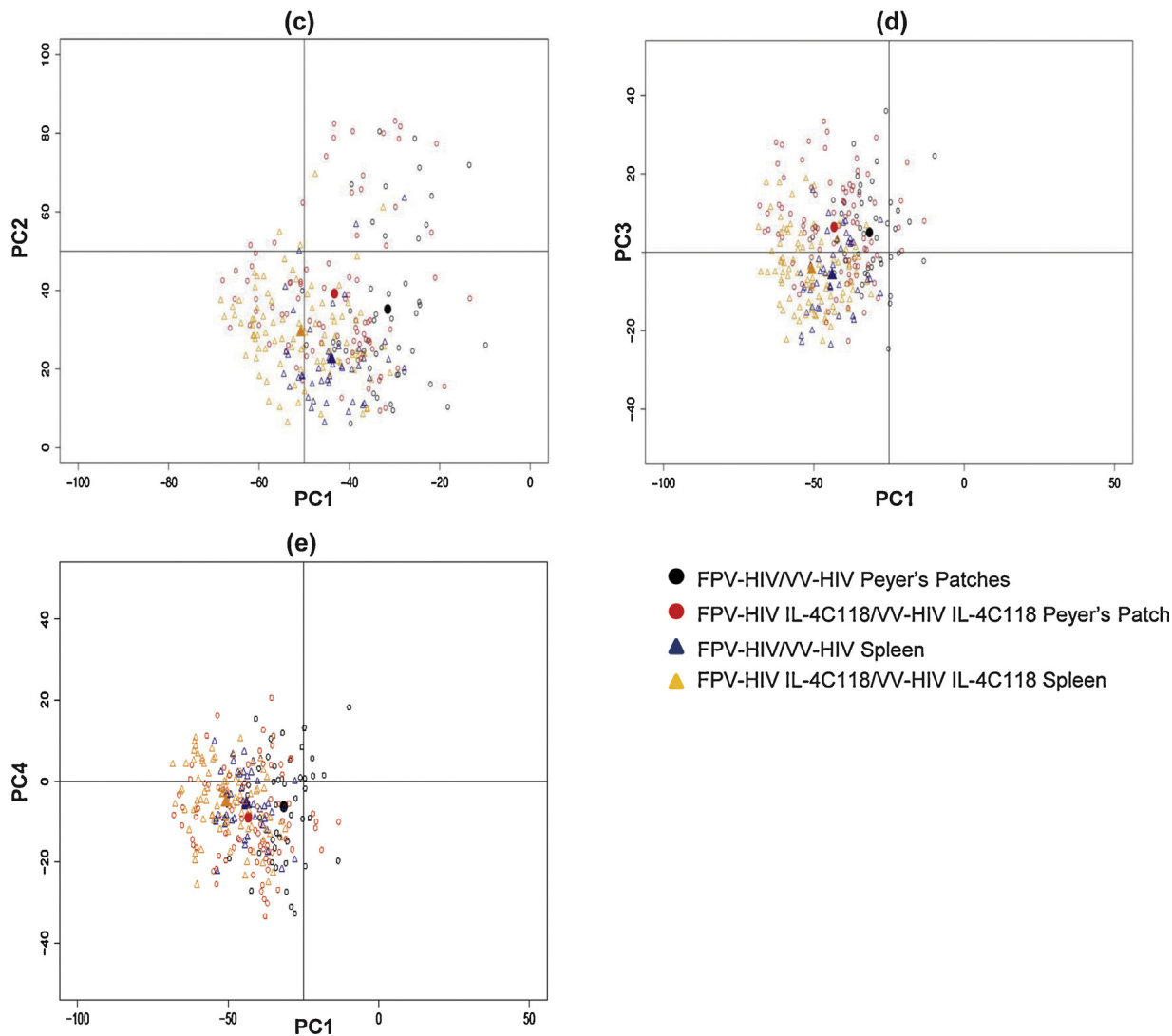


Fig. 5. (Continued).

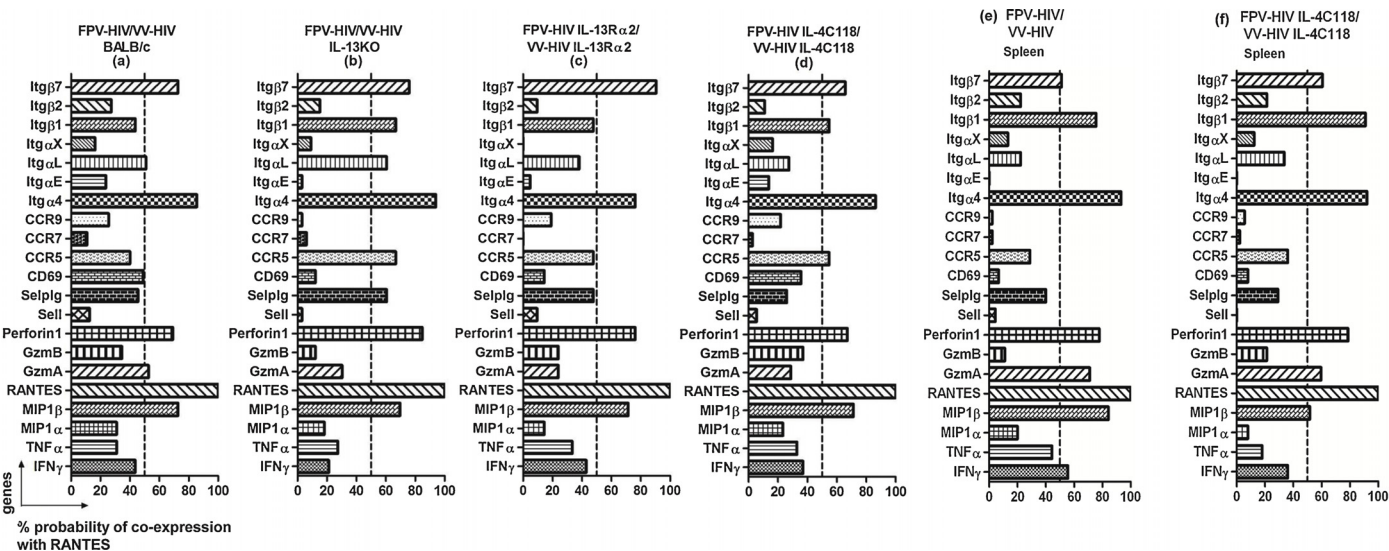


Fig. 6. Following different vaccinations, analysis of genes that were co-expressed with RANTES within K^dGag_{197–205}-specific single CD8⁺ T cells. BALB/c and IL-13 KO mice were immunized i.n./i.m. with different vaccines as indicated (a–f), cells expressing RANTES were considered 100% and then the percentage probability of indicated genes co-expressed with RANTES in Peyer's patch (a–d) and spleen (e and f) were determined using Matlab software as indicated in Section 2. Data represent two experiments for standard unadjuvanted vaccine and IL-4R antagonist adjuvanted vaccine and one experiment for IL-13 KO and IL-13Rα2 adjuvant vaccine group. Note: Data presented in Figs. 1–6 were obtained from same vaccination experiment.

cells that expressed RANTES were also found to co-express MIP1- β , perforin, integrin $\alpha 4$ and $\beta 7$ (Fig. 6e and f) and granzyme-A and integrin $\beta 1$ were found to be greatly elevated in spleen compared to Peyer's patch (Fig. 6a, e and d, f).

Overall quantitative analysis of the data indicates that integrin αE (Fig. 3) and CCR9 (Figs. 3–6) were specific to Peyer's patch, and higher proportion and relative higher expression of granzyme A (Figs. 3–6) and integrin $\beta 2$ (Figs. 3–5) were detected in spleen compared to Peyer's patches. However, RANTES, MIP1- β , perforin, integrin $\alpha 4$, $\beta 1$ and $\beta 7$ (Figs. 1–6) were found to be common biomarkers detected both in Peyer's patch and spleen (see Venn diagram Supplementary Fig. 2).

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4. Discussion

In the current study, 21 out of the 30 mRNAs tested were differentially expressed between unadjuvanted i.n. FPV-HIV/i.m. VV-HIV vaccine group compared to novel IL-13R $\alpha 2$ and IL-4R antagonist adjuvanted vaccinated groups that have shown to induce high-avidity/poly-functional mucosal and systemic K^dGag_{197–205}-specific CD8⁺ T-cell immunity [34,35]. The cytokine expression by gut or splenic-K^dGag_{197–205}-specific single CD8⁺ T cells was not significantly different between the groups, which is not entirely surprising as unstimulated (no peptide/protein encountered) K^dGag_{197–205}-specific CD8⁺ T cells have shown to express no or very low IFN- γ , TNF- α and IL-2 at the mRNA and proteins levels [2,22]. Multiple studies have shown that following vaccination measuring the expression of not only cytokines (i.e. IFN- γ) but also chemokines, granzymes and perforin is of great importance when evaluating vaccine efficacy [24,41]. The principal component analysis of gut-K^dGag_{197–205}-specific single cells revealed enhanced expression of RANTES and MIP-1 β mRNA following IL-13R $\alpha 2$ and IL-4R antagonist adjuvanted vaccination strategy including the IL-13KO mice given the unadjuvanted vaccine compared to the BALB/c unadjuvanted control. This is consistent with our previous finding where elevated RANTES was detected in IL-13^{−/−} and IL-4^{−/−} splenic K^dGag_{197–205}-specific CD8⁺ T cells following unadjuvanted vaccination [22]. Macaques vaccinated with SHIV-4, the expression of RANTES together with IFN- γ , have been associated with protection against SIVsm challenge [26]. Involvement of RANTES in protection has also been reported with other chronic viral infections [42]. Moreover, in HIV non-progressors not only high levels of IFN- γ and [24] MIP-1 β but also expression of perforin by HIV-specific CD8⁺ T cells has been reported [43,44]. PCA analysis revealed that unlike IL-13R $\alpha 2$ adjuvanted vaccine where IL-13 was transiently inhibited, complete lack of IL-13 (IL-13 KO group) not only increased RANTES, MIP-1 β , and perforin mRNA expression by gut-K^dGag_{197–205}-specific CD8⁺ T cells but also increased the levels of granzymes A and B mRNA expression. [Note that although the “number” of gut-K^dGag_{197–205}-specific single CD8⁺ T cells that expressed granzymes A and B were lower in all four vaccination groups tested, the “level of expression” was significantly elevated in IL-13KO mice that received the control unadjuvanted vaccine, which is consistent with our previous findings [2].] It is now established that enhanced expression of perforin and granzymes by CD8 T cells correlate with enhanced cytotoxicity and vaccine-specific protective efficacy [30,45–47]. We have

found that IL-13 KO mice given the control unadjuvanted vaccine were more protected against a surrogate mucosal influenza-HIV challenge compared to BALB/c mice given the IL-13R $\alpha 2$ adjuvanted vaccine. This difference in protection in IL-13 KO mice could mainly be associated with the enhanced expression of RANTES, MIP-1 β , perforin and also granzymes A and B by these K^dGag_{197–205}-specific CD8⁺ T cells at the mucosae (enhanced expression of cytotoxic proteins). Interestingly, PCA revealed that the mean PC2 scores differed significantly between the IL-13 KO and the novel vaccine groups tested, highlighting the unique effects of transient inhibition of IL-13 versus total absence of IL-13 activity at the mucosae.

It is established that migration of lymphocytes to gut mucosae is mediated by integrin $\alpha 4$ heterodimerisation with $\beta 7$ chain, not the $\beta 1$ chain, and MAdCAM-1 ligand interacts preferentially with $\alpha 4\beta 7$, not $\alpha 4\beta 1$ [11,48], which is also consistent with our recent findings [68] Following the adjuvanted and unadjuvanted vaccination, relatively higher numbers of gut K^dGag_{197–205}-specific CD8⁺ T cells were found to express $\beta 7$ but not $\beta 1$ mRNA, indicating that higher numbers of antigen-specific CD8⁺ T cells could be trafficking to the gut mucosae. This is of importance in the context of an HIV vaccine, as the primary site of CD4 depletion is thought to be the gut mucosae [49,50]. In contrast, in all groups tested, increased numbers of $\beta 1$ expressing splenic-K^dGag_{197–205}-specific CD8⁺ T cells as well as elevated expression of $\beta 1$ mRNA and protein were detected in splenic-K^dGag_{197–205}-specific compared to Peyer's patch, suggesting that in spleen integrin $\beta 1$ preferentially heterodimerised with integrin $\alpha 4$ and not integrin $\beta 7$. Interestingly, in CD4⁺ T cells, elevated expression of $\beta 1$ integrin subunit has shown to hamper integrin $\beta 7$ interaction with integrin $\alpha 4$, resulting in suppression of $\alpha 4\beta 7$ protein expression and T-cell homing to Peyer's patch [51]. Recently, using single-cell analysis, Kim et al. also have demonstrated that the co-engagement of $\alpha 4\beta 1$ together with CD8/CD4 co-receptors on human T cells can also induce robust IL-2 and IFN- γ cytokine production [52]. Elevated IL-2 and IFN- γ expression by splenic-K^dGag_{197–205}-specific CD8⁺ T cells (post HIV-peptide stimulation) have been detected in adjuvanted vaccinated group compared to mice given the unadjuvanted strategy [34,35]. These findings further indicate that integrin $\beta 1$ may not only play a role in T-cell trafficking but also optimal T-cell activation and effector function.

In murine and non-human primate models, differential regulation of immune responses has been observed in systemic and mucosal compartments [37,53–56]. Consistent to other studies [57–59], our current data further confirm that there is a clear compartmentalization of immune responses between the spleen and gut compartments, even at the single cell level, highlighting the importance of evaluating both systemic and mucosal immunity, following mucosal vaccination. We believe that these differences are mainly linked to (i) the cytokine cell milieu induced following vaccination [2,68] and (ii) the resulting innate lymphoid cell subsets and antigen presenting cell subsets activated at the vaccination site [35,60], (iii) the mode of antigen uptake and presentation that take place via M-cells, which is exclusive to the mucosae [61,62], (iv) plus the homing signature acquired by the resulting T cells according to the anatomical location [68,63]. For example, it has been shown that priming with Peyer's patch derived DCs (but not splenic DCs) can induce the up-regulation of $\alpha 4\beta 7$ and CCR9 on CD8⁺ T cells and licence them to migrate to the gut mucosae [64]. In this study, although $\beta 7$ mRNA and $\alpha 4\beta 7$ protein expression levels were similar in splenic or Peyer's patch derived K^dGag_{197–205}-specific CD8⁺ T cells, significantly elevated CCR9 expression was detected only in gut. Interestingly, PCA revealed a negative correlation of integrin $\alpha 4$ and CCR9 mRNA expression. MAdCAM-1 (which binds to $\alpha 4\beta 7$) which is mainly detected in high endothelial venules of Peyer's patch is also thought to be present on

the sinus-lining cells in the spleen [65]. Thus, this may explain the unexpected abundance of $\alpha 4\beta 7^+$ K^dGag_{197–205}-specific splenic CD8⁺ T cells observed, suggesting these may originate from gut (circulating gut T cells) [66]. In contrast, epithelial cells in the small intestine exclusively express the chemokine ligand 25 (CCL25), which can bind to CCR9 on T cells, thereby facilitating CCR9⁺ T-cell homing to the intestine [67]. Thus, the current data indicated that compared to $\alpha 4\beta 7$, CCR9 is more specifically involved in gut-homing of HIV-specific CD8⁺ T cells. Moreover, correlated expression of CCR9 and integrin αE was also established by PCA. Interestingly, expression of these two molecules was only detected in gut-K^dGag_{197–205}-specific single CD8⁺ T cells, suggesting CCR9 and integrin αE could play a role in migration as well as retention of CD8⁺ T cell in the intestinal mucosae [10]. It will be of interest to evaluate this homing marker expression at various mucosal effector sites.

Data indicate that where sample size is limited, single cell Fluidigm 48.48 Dynamic arrays can be successfully used to evaluate vaccine-specific mucosal immunity. The PCA demonstrated that novel IL-13R $\alpha 2$ and IL-4R antagonist adjuvanted vaccines were uniquely different compared to the WT BALB/c control or IL-13KO groups given the unadjuvanted vaccine, indicating that level of IL-13 inhibition (total, transient or no inhibition) can significantly modulate the level of poly-functionality/cytotoxicity of CD8⁺ T cells, altering the degree of T cell-mediated protective efficacy. The distinct clustering pattern of the spleen and gut K^dGag_{197–205}-specific single CD8⁺ T cells, following PCA, also revealed that according to the anatomical location the mRNA expression profiles of the 21 genes tested can be significantly different, including Em and Cm T-cell ratios. Collectively, our analysis of the (i) relative numbers of cells expressing the mRNAs, (ii) poly-functionality in relation to RANTES expression and (iii) level of mRNA expression using PCA indicated that RANTES, MIP-1 β , perforin and integrins $\alpha 4$, $\beta 1$ and $\beta 7$ could be used as a set of biomarkers to measure effective vaccine-specific mucosal immunity in HIV-specific single T cells obtained from mucosal or systemic compartments.

Author contributions

S.T. conducted all the experiments, a part of data analysis and prepared the manuscript, C.J. and T.N. performed the PCA and statistical analysis, R.R. developed and applied the Matlab code, R.J.J. designed and constructed all the rFPV, rVV, IL-13Ra2 and IL-4R α antagonist adjuvanted vaccines, and C.R. helped design all the experiments and critical evaluation and preparation of the manuscript.

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Conflict of interest: The authors have no conflicts of interest.

Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at <http://dx.doi.org/10.1016/j.vaccine.2015.10.085>.

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